

1/21  
**FcR-I**

1	GCAGGAATTGGCACGGCTCTGTCTGCCAGCAGGAGGGCTATCCATCCACAGAGC	60
61	AGTGCAGTGGGAGGAGACGCCATGACCCCCATCCTCACGGTCTGATCTGTCTCGGGCCC	120
1	M T P I L T V L I C L G P	13
121	CTCCCCAAGCCCACCCCTCTGGGCTGAGCCAGGCTCTGTGATCACCAAGGGAGTCCTGTG	180
14	L P K P T L W A E P G S V I T Q G S P V	33
181	ACCTCAGGTGTCAGGGAGCCTGGAGACGCAGGAGTACCATCTATATAAGAAAAGAAA	240
34	T L R C Q G S L E T Q E Y H L Y R E K K	53
241	ACAGCACTCTGGATTACACGGATCCCACAGGAGCTGTGAAGAAGGGCCAGTTCCCATC	300
54	T A L W I T R I P Q E L V K K G Q F P I	73
301	CTATCCATCACCTGGAACATGCAGGGCGGTATTGCTGTATCTATGGCAGCCACACTGCA	360
74	L S I T W E H A G R Y C C I Y G S H T A	93
361	GGCCTCTCAGAGAGCAGTGACCCCTGGAGCTGGTGGTACAGGAGCCTACAGCAAACCC	420
94	G L S E S S D P L E L V V T G A Y S K P	113
421	ACCCTCTCAGCTCTGCCAGCCCTGTGGTGACCTCAGGAGGAAATGTGACCATCCAGTGT	480
114	T L S A L P S P V V T S G G N V T I Q C	133
481	GACTCACAGGTGGCATTGATGGCTTCATTCTGTGTAAGGAAGGAGAAGATGAACACCCA	540
134	D S Q V A F D G F I L C K E G E D E H P	153
541	CAATGCCTGAACCTCCATTCCATGCCGTGGTCATCCGGGCCATCTCTCCGTGGC	600
154	Q C L N S H S H A R G S S R A I F S V G	173
601	CCCGTGAGCCCAAGTCGCAGGTGGTCGTACAGGTGCTATGGTTATGACTCGCGCGCTCCC	660
174	P V S P S R R W S Y R C Y G Y D S R A P	193
661	TATGTGTGGTCTCTACCCAGTGATCTCTGGGCTCTGGTCCCAGGTGTTCTAAGAAG	720
194	Y V W S L P S D L L G L L V P G V S K K	213
721	CCATCACTCTCAGTGCAGCCGGTCTGTCGTGGCCCTGGGGAGAAGCTGACCTCCAG	780

**FIG. 1A**

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**FcR-I**

214	P S L S V Q P G P V V A P G E K L T F Q	233
781	TGTGGCTCTGATGCCGGCTACGACAGATTGTTCTGTACAAGGAGTGGGACGTGACTTC	840
234	C G S D A G Y D R F V L Y K E W G R D F	253
841	CTCCAGCGCCCTGGCCGGCAGCCCCAGGCTGGCTCTCCCAGGCCAACTTCACCCGGC	900
254	L Q R P G R Q P Q A G L S Q A N F T L G	273
901	CCTGTGAGCCGCTCCTACGGGGCCAGTACACATGCTCCGGTGCATAAACCTCTCC	960
274	P V S R S Y G G Q Y T C S G A Y N L S S	293
961	GAGTGGTCGGCCCCAGCGACCCCTGGACATCCTGATCACAGGACAGATCCGTGCCAGA	1020
294	E W S A P S D P L D I L I T G Q I R A R	313
1021	CCCTTCCCTCCGTGCGGCCGGCCCCACAGTGGCTCAGGAGAGAACGTGACCCCTGCTG	1080
314	P F L S V R P G P T V A S G E N V T L L	333
1081	TGTCAGTCACAGGGAGGGATGCACACTTCCCTTTGACCAAGGAGGGCAGCTGATTCC	1140
334	C Q S Q G G M H T F L L T K E G A A D S	353
1141	CCGCTGCGTCTAAATCAAAGCGCCAATCTCATAGTACCAGGCTGAATTCCCCATGAGT	1200
354	P L R L K S K R Q S H K Y Q A E F P M S	373
1201	CCTGTGACCTCGGCCACGCGGGGACCTACAGGTGCTACGGCTCACTCAGCTCCAACCC	1260
374	P V T S A H A G T Y R C Y G S L S S N P	393
1261	TACCTGCTGACTCACCCAGTGACCCCTGGAGCTCGTGGTCTCAGGAGCAGCTGAGACC	1320
394	Y L L T H P S D P L E L V V S G A A E T	413
1321	CTCAGCCCACCAAAACAAGTCCGACTCCAAGGCTGGTGAGTGAGGAGATGCTTGGCGT	1380
414	L S P P Q N K S D S K A G E *	427
1381	GATGACGCTGGGCACAGAGGGTCAGGTCTGTCAAGAGGAGCTGGGTGTCCTGGTGGAC	1440
1441	ATTTGAAGAATTATTCATTCAACTTGAAGAATTATTCAACACCTTAACAATGTATA	1500
1501	TGTGAAGTACTTATTCTTCATATTTAAAAATAAAAGATAATTATCCATG	1552

**FIG. 1B**

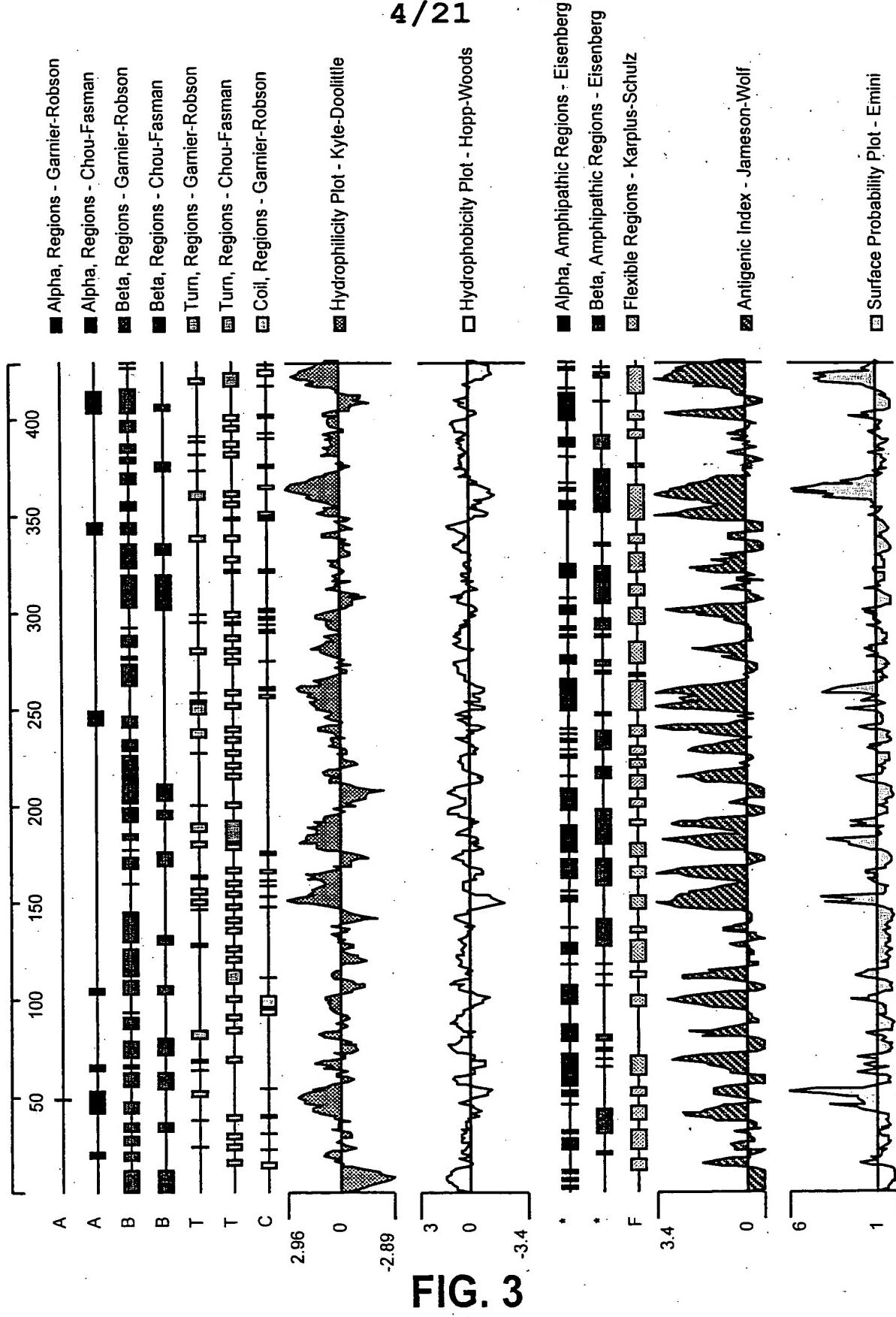
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Percent Similarity: 63.090

Percent Identity: 45.064

HMQDO20.aa x FCg2RBos.aa

**FIG. 2**



**FcRII**

1	ACCCACGCGTCCGCACTCTAGCGGTATCTGCCACCATGGCCCTGGTGCTGATCCTCCAG	60
1	<u>M A L V L I L O</u>	8
61	CTGCTGACCCCTCTGGCCTCTGTGTACACAGACATCACTCCGTCTGTCCCCCAGCTTCA	120
9	<u>L L T L W P L C H T D I T P S V P P A S</u>	28
121	TACCACCCATAAGCCATGGCTGGGAGCTCAGCCGGCTACAGTTGTGACCCCTGGGTCAAC	180
29	<u>Y H P K P W L G A Q P A T V V T P G V N</u>	48
181	GTGACCTTGAGATGCCGGCACCCAAACCCGCTTGGAGATTGGACTTTCAAGCCTGGA	240
49	<u>V T L R C R A P Q P A W R F G L F K P G</u>	68
241	GAGATCGCTCCCTTCTCTCCGGATGTGTCCTCCGAGCTGGCAGAATTCTTCTGGAG	300
69	<u>E I A P L L F R D V S S E L A E F F L E</u>	88
301	GAGGTGACTCCAGCCAAGGGGGAAAGTTACCGCTGCTGCTACCGAAGGCCAGACTGGGG	360
89	<u>E V T P A Q G G S Y R C C Y R R P D W G</u>	108
361	CCGGGTGTCTGGTCCCAGCCAGCGATGTGTCCTGGAGCTGCTGGTGACAGAGGAGCTGCCG	420
109	<u>P G V W S Q P S D V L E L L V T E E L P</u>	128
421	CGGCCGTCGCTGGTGGCGCTGCCGGGGCGGTGGTGGTCCCTGGCGCCAACGTGAGCCTG	480
129	<u>R P S L V A L P G P V V G P G A N V S L</u>	148
481	CGCTGCGGGGCCCTGCGAACATGAGCTCGTGTACCCGAGGGCGTGGCGGC	540
149	<u>R C A G R L R N M S F V L Y R E G V A A</u>	168
541	CCGCTGCAGTACCGCCACTCCGCGAGCCCTGGGCCGACTTCACGCTGCTGGCGCCCGC	600
169	<u>P L Q Y R H S A Q P W A D F T L L G A R</u>	188
601	GCCCCCGGCACCTACAGCTGCTACTATCACACGCCCTCCGCGCCCTACGTGCTGTGCAG	660
189	<u>A P G T Y S C Y Y H T P S A P Y V L S Q</u>	208

**FIG. 4A**

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**FcRII**

661	CGCAGCGAGGTGCTGGTCATCAGCTGGGAAGACTCTGGCTCCTCCGACTACACCCGGGG	720
209	R S E V L V I S W E D S G S S D Y T R G	228
721	AACCTAGTCCGCCTGGGGCTGGCCGGCTGGTCCTCATCTCCCTGGCGCGCTGGTCACT	780
229	N L V R L G L A G L V L I S L G A L V T	248
781	TTTGACTGGCCCAGTCAGAACCGCGCTCTGCTGGTATCCGCCCTGAGCCCCAGGAGCA	840
249	F D W R S Q N R A P A G I R P *	263
841	CTGCAGCCCGAGACTTCCAACCTGAGTGGCGGAGAAGCTGGGACCCCTGGGCTGGACTGTC	900
901	CTTCCCTGCAGCCCCACAGTCCTGCTGGCTGAGCTCCGCGAACGGTCCTTAGACCCCGC	960
961	TGTGCCCTGTGCTGTAGCTTCTTCCAGGCCTTCCAAGGAGTAGCTGAAAGGAAGACG	1020
1021	CGATTAGTGGTTAAGACTTCCAAGCCAGAACAGACAGAGGGTTCGAATCCCAGCACTGCCGT	1080
1081	CTACTCACTGTAGTAGCTAGCAGCTACAGAAAGGTAGTAGTGAGACGTGAAGCCAGCTGGA	1140
1141	CTTCCTGGGTTGAATGGGGACCTGGAGAACCTTCTGCTTACAAGAGGATTGTAAAATG	1200
1201	GACCAATCAGCACTCTGTAAGATGGACCAATCAGCGCTCTGTAAAATGGACCAATCAGCA	1260
1261	GGACATGGCGGGGACAATAAGGAATAAAAGCTGGCGAGCGCGGCACCCACCAGAGTC	1320
1321	TGCTTCCACGCTGTGGGAGCTTGTCTTGCTCTACACAATAATCTGCTGCTGCTA	1380
1381	AAAAAAAAAAAAAAAAAAAAAA	1410

**FIG. 4B**

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**Percent Similarity: 54.400**

**Percent Identity: 37.600**

**HDPMK33.aa x FCg2RBos.aa**

5 LILQLLTLWPLCHTDITPSVPPASYHPKPWLGAQPATVVTPGVNVTLRCR 54

: | .|:.|.. . . .|. : ||| : |:|..||. | .||: |.

1 MAPTLPALLCLGLSVGLRTQVQAGTFPKPIIWAEPSSVPLGSSVTILCQ 50

55 APQPAWRFGLFKPGEIAPLLFRDV..SSELAEFFLEEVTPAQGGSYRCCY 102

:|.|...||:|.|: .|: ::. . .: |||:..:| ..|:|.||:|.

51 GPPNTKSFSLNKEGDSTPWNIHPSLEPWDKANFFISNVREQQAGRYHCS. 99

103 RRPDWGPGWWSQPSDVLELLVTELP.....RPSLVALPGPVVGPGANV 146

.: .. ||:||:.:|:|||..| | | | | . |:| |:|||.||.

100 ...HFIGVNWSEPSEPLDLLVAGEEPAGRLRDRPSLSVRSPSPSVAPGENV 146

147 SLRCAGRLRNMSFVLYREGVAA.PLQYRHSQ...WADFTL..LGARAP 190

.| |.: |. .|:| :|||. | |..| .|. |:|. | ... .

147 TLLCQSGNRTDTFLSKEGAHRPLRLRSQDQDGWYQAEFSLSPVTSAHG 196

191 GTYSCYYHTPSAPYVLSQRSEVLVISWEDSGSSDYTRGNLVRLGLAGLVL 240

|||.|| | ...||:|||.|||. |: .|||..|||:|||:||

197 GTYRCYRSLSTNPYLLSQPSEPLALL.....VADYTMQNLIRMGGLAASVL 241

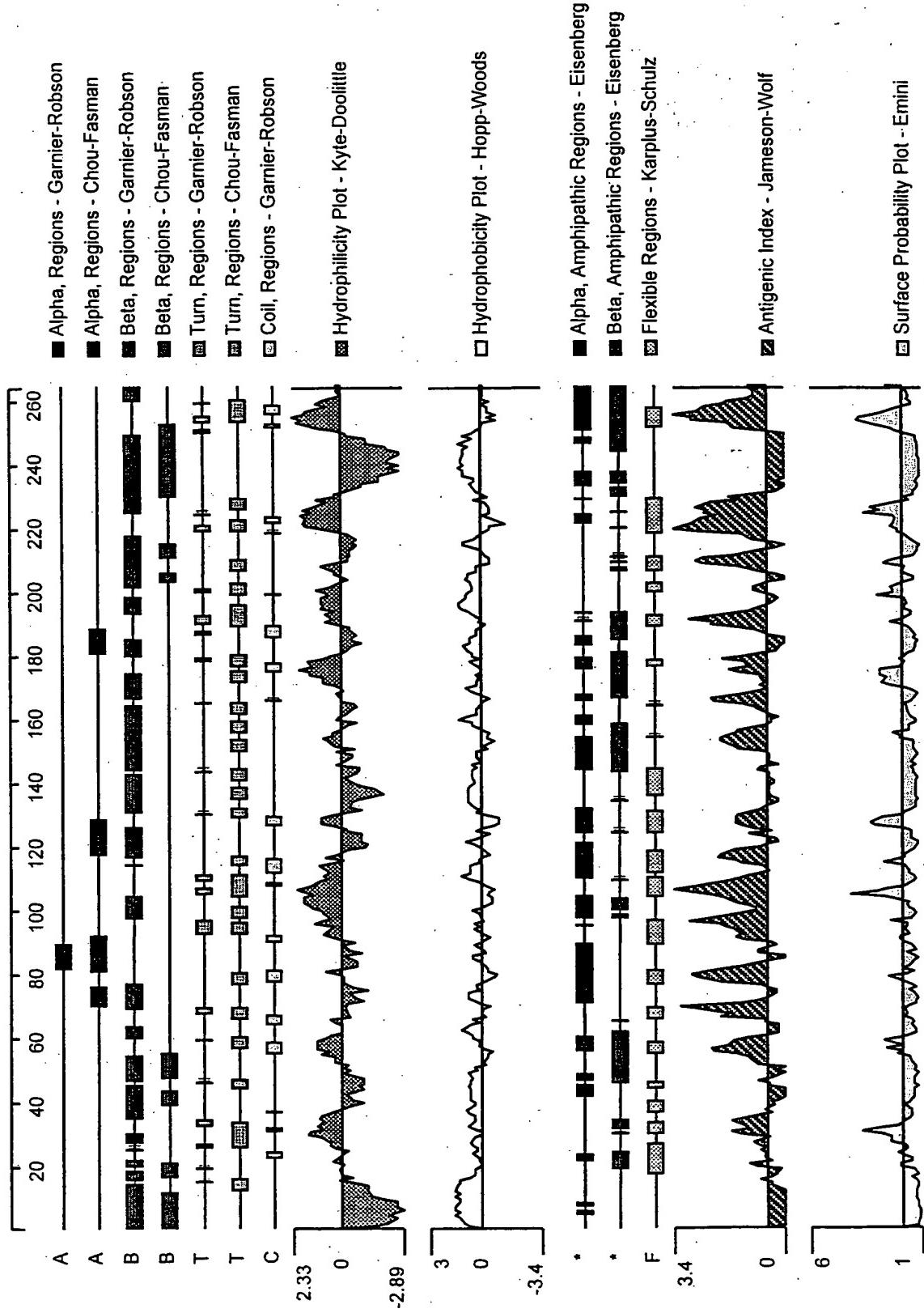
241 ISLGALVTFDWRSQNRAPAGIRP 263

:|| |:.. .:::. |..: |.

242 LLGILLCQARHDHGGAREAARS 264

**FIG. 5**

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**FIG. 6**

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**FcR-III**

1	GCAGGAATTGGCACGAGCAGCACTGAGGGCTCATCCCTCTGCAGAGCGCGGGGTACCG	60
61	GAAGGAGACGCCATGACGCCCGCCCTCACAGCCCTGCTCTGCCTTGGCTGAGTCTGGC	120
1	M T P A L T A L L C L G L S L G	16
121	CCCAGGACCCGCGTGCAGGCAGGGCCCTTCCCCAAACCCACCCCTCTGGCTGAGCCAGGC	180
17	P R T R V Q A G P F P K P T L W A E P G	36
181	TCTGTGATCAGCTGGGGAGCCCCGTGACCATCTGGTGTCAAGGGAGCCTGGAGGCCAG	240
37	S V I S W G S P V T I W C Q G S L E A Q	56
241	GAGTACCAACTGGATAAAGAGGGAAAGCCCAGAGCCCTGGACAGAAATAACCCACTGGAA	300
57	E Y Q L D K E G S P E P L D R N N P L E	76
301	CCCAAGAACAAAGGCCAGATTCTCCATCCCATCCATGACACAGCACCATGCAGGGAGATA	360
77	P K N K A R F S I P S M T Q H H A G R Y	96
361	CGCTGCCACTATTACAGCTCTGCAGGCTGGTCAGAGCCAGCGACCCCTGGAGCTGGT	420
97	R C H Y Y S S A G W S E P S D P L E L V	116
421	ATGACAGGAGCCTATAGCAAACCCACCCCTCTCAGCCCTGCCAGCCCTGTGGTGCCTCA	480
117	M T G A Y S K P T L S A L P S P V V A S	136
481	GGGGGGAAATATGACCCCTCGATGTGGTCACAGAAGAGATATCACCATTGTTCTGATG	540
137	G G N M T L R C G S Q K R Y H H F V L M	156
541	AAGGAAGGGAGAACACCAGCTCCCCGGACCCCTGGACTCACAGCAGCTCCACAGTGGGGG	600
157	K E G E H Q L P R T L D S Q Q L H S G G	176
601	TTCCAGGCCCTGTTCCCTGTGGGCCCCGTGAACCCACAGGCCACAGGTGGAGGTTACATG	660
177	F Q A L F P V G P V N P S H R W R F T C	196

**FIG. 7A**

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**FcR-III**

661	TATTACTATTATGAAACACCCCCCGGGTGTGGTCCCACCCAGTGACCCCTGGAGATT	720
197	Y Y Y Y M N T P R V W S H P S D P L E I	216
721	CTGCCCTCAGGCGTGTCTAGGAAGCCCTCCCTCCTGACCTGCAGGGCCCTGTCCCTGGCC	780
217	L P S G V S R K P S L L T L Q G P V L A	236
781	CCTGGGCAGAGCCTGACCCCTCCAGTGTGGCTCTGATGTGGCTACGACAGATTGTTCTG	840
237	P G Q S L T L Q C G S D V G Y D R F V L	256
841	TATAAGGAGGGGAACGTGACTTCCTCCAGGCCCTGGCCAGCAGCCCCAGGCTGGCTC	900
257	Y K E G E R D F L Q R P G Q Q P Q A G L	276
901	TCCCAGGCCAACTTCACCCCTGGGCCCTGTGAGCCCTCCAATGGGGCCAGTACAGGTGC	960
277	S Q A N F T L G P V S P S N G G Q Y R C	296
961	TACGGTGCACACAACCTCTCCTCCGAGTGGTCGGCCCCAGCGACCCCTGAACATCCTG	1020
297	Y G A H N L S S E W S A P S D P L N I L	316
1021	ATGGCAGGACAGATCTATGACACCGTCTCCCTGTCAAGCACAGCCGGCCCCACAGTGGCC	1080
317	M A G Q I Y D T V S L S A Q P G P T V A	336
1081	TCAGGAGAGAACGTGACCCCTGCTGTGTCACTGGTGGCAGTTGACACTTCCTCTG	1140
337	S G E N V T L L C Q S W W Q F D T F L L	356
1141	ACCAAAGAAGGGCAGCCCACCCCCACTGCGTCTGAGATCAATGTACGGAGCTCATAG	1200
357	T K E G A A H P P L R L R S M Y G A H K	376
1201	TACCAGGCTGAATTCCCCATGAGTCCTGTGACCTCAGCCCACGCCGGGACCTACAGGTGC	1260
377	Y Q A E F P M S P V T S A H A G T Y R C	396
1261	TACGGCTCACGCAGCTCAACCCCTACCTGCTGTCTACCCAGTGAGCCCCCTGGAGCTC	1320
397	Y G S R S S N P Y L L S H P S E P L E L	416

**FIG. 7B**

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**FcR-III**

1321	GTGGTCTCAGGACACTCTGGAGGCTCCAGCCTCCCACCCACAGGGCCGCCCTCCACACCT	1380
417	V V S G H S G G S S L P P T G P P S T P	436
1381	GGTCTGGGAAGATACTGGAGGTTTGATTGGGGTCTCGGTGGCCTCGTCCTGCTGCTC	1440
437	G L G R Y L E V L I G V S V A F V L L L	456
1441	TTCCCTCCTCCTCTTCCTCCTCCGACGTCAAGCTCACAGCAAACACAGGACATCTGAC	1500
457	F L L L F L L L R R Q R H S K H R T S D	476
1501	CAGAGAAAGACTGATTCCAGCGCTCTGCAGGGCTGCAGGAGACAGAGCCAAAGGACAGG	1560
477	Q R K T D F Q R P A G A A E T E P K D R	496
1561	GGCCTGCTGAGGAGGTCCAGCCCAGCTGCTGACGTCCAGGAAGAAAACCTCTATGCTGCC	1620
497	G L L R R S S P A A D V Q E E N L Y A A	516
1621	GTGAAGGACACACAGTCTGAGGACGGGTGGAGCTGGACAGTCAGAGCCCACACGATGAA	1680
517	V K D T Q S E D G V E L D S Q S P H D E	536
1681	GACCCCCACGCAGTGACGTATGCCCGGTGAAACACTCCAGTCCTAGGAGAGAAATGGCC	1740
537	D P H A V T Y A P V K H S S P R R E M A	556
1741	TCTCCTCCTCCCCACTGTCTGGGAATTCTGGACACAAAGGACAGACAGGCAGAAGAG	1800
557	S P P S P L S G E F L D T K D R Q A E E	576
1801	GACAGACAGATGGACACTGAGGCTGCTGCATCTGAAGCCTCCCAGGATGTGACCTACGCC	1860
577	D R Q M D T E A A A S E A S Q D V T Y A	596
1861	CAGCTGCACAGCTTGACCCCTAGACGGAAGGCAACTGAGCCTCTCCATCCCAGGAGTTC	1920
597	Q L H S L T L R R K A T E P P P S Q E F	616
1921	GAGTCAGTCAGATCAGCATTGTGAGGCCCATCTCTACAAAAATAAAACCAGTCCGGCG	1980
617	E S V R S A L *	623

1981 TGGTGGCACAA 1991

**FIG. 7C**

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Percent Similarity: 69.697

Percent Identity: 53.788

HMPAP73.aa x FCg2RBos.aa

**FIG. 8**

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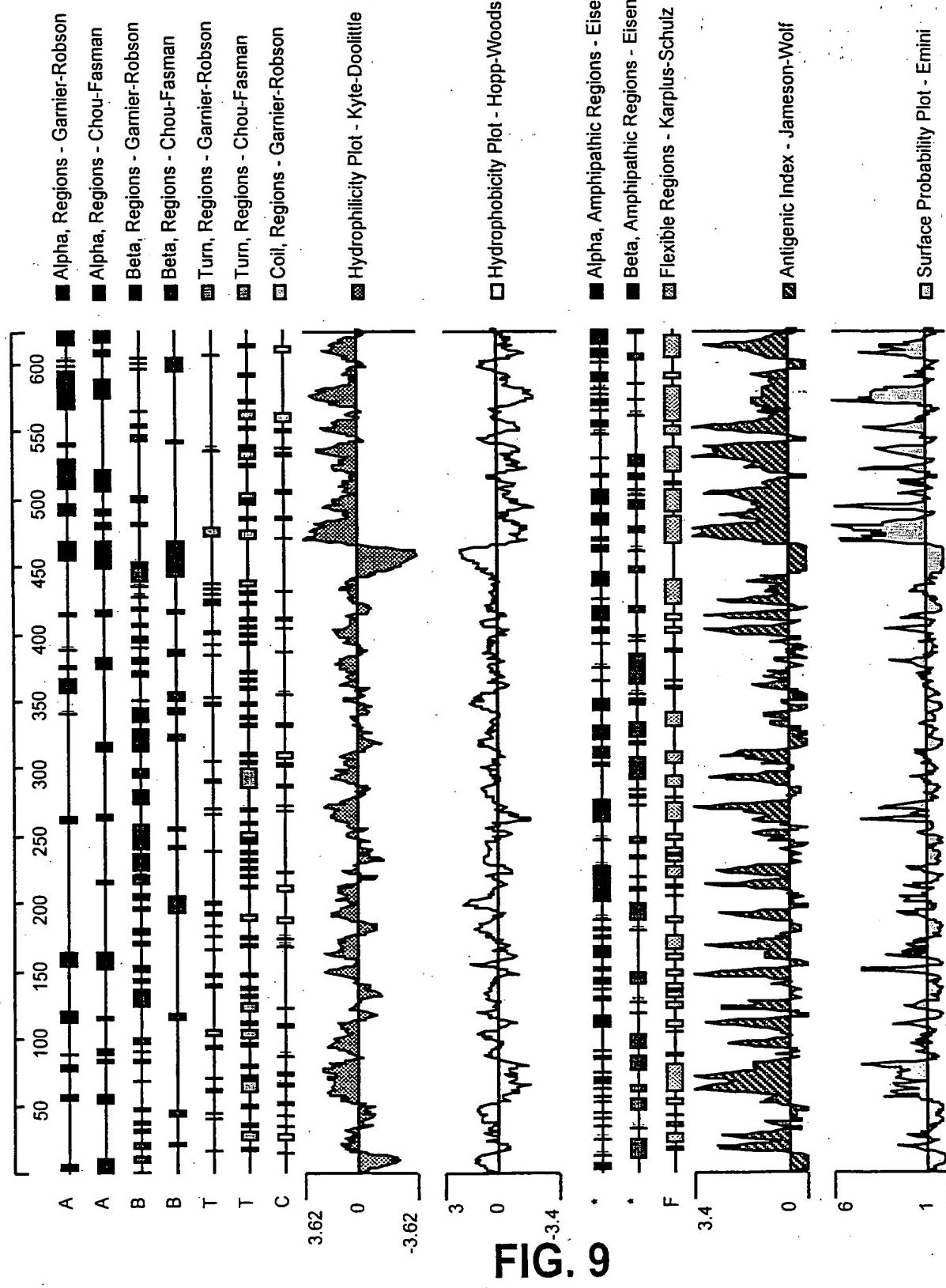


FIG. 9

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**FcR-IV**

1	GGAATTCCGGGAGGAGACGCCATGATCCCCACCTTCACGGCTCTGCTCTGCCTCGGGCTG	60
1	<u>M I P T F T A L L C L G L</u>	13
61	AGTCTGGGCCCACTACCCACATGCAGGCAGGGCCCTCCCCAAACCCACCCCTCTGGGCT	120
14	<u>S L G P S T H M Q A G P L P K P T L W A</u>	33
121	GAGCCAGGCTCTGTGATCAGCTGGGGAACTCTGTGACCATCTGGTGTCAAGGGACCCCTG	180
34	E P G S V I S W G N S V T I W C Q G T L	53
181	GAGGCTCGGGAGTACCGTCTGGATAAAGAGGAAAGCCCAGCACCCCTGGGACAGACAGAAC	240
54	E A R E Y R L D K E E S P A P W D R Q N	73
241	CCACTGGAGCCAAGAACAAAGGCCAGATTCTCCATCCCATCCATGACAGAGGACTATGCA	300
74	P L E P K N K A R F S I P S M T E D Y A	93
301	GGGAGATAACCGCTTTACTATCGCAGCCCTGAGGCTGGTCACAGCCCAGTGACCCCCCTG	360
94	G R Y R C Y Y R S P V G W S Q P S D P L	113
361	GAGCTGGTGATGACAGGAGCCTACAGTAAACCCACCCCTTCAGCCCTGCCAGTCCTCTT	420
114	E L V M T G A Y S K P T L S A L P S P L	133
421	GTGACCTCAGGAAAGAGCGTGACCCCTGCTGTGTCAGTCACGGAGCCAAATGGACACTTTT	480
134	V T S G K S V T L L C Q S R S P M D T F	153
481	CTTCTGATCAAGGAGGGGCAGCCATCCCCACTGCATCTGAGATCAGAGCACGGAGCT	540
154	L L I K E R A A H P L L H L R S E H G A	173
541	CAGCAGCACCAAGGCTGAATTCCCCATGAGTCCTGTGACCTCAGTGCACGGGGGACCTAC	600
174	Q Q H Q A E F P M S P V T S V H G G T Y	193
601	AGGTGCTTCAGCTCACACGGCTCTCCACTACCTGCTGTCAACACCCAGTGACCCCCCTG	660
194	R C F S S H G F S H Y L L S H P S D P L	213
661	GAGCTCATAGTCTCAGGATCCTGGAGGGTCCAGGCCCTCACCCACAAGGTCCGTCTCA	720
214	E L I V S G S L E G P R P S P T R S V S	233

**FIG. 10A**

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FcR-IV

721	ACAGCTGCAGGCCCTGAGGACCAGCCCCATGCCTACAGGGTCAGTCCCCACAGTGGT	780
234	T A A G P E D Q P L M P T G S V P H S G	253
781	CTGAGAAGGCAGTGGAGGTACTGATCGGGGCTTGGTGGCTCCATCCTGCTTCTCC	840
254	L R R H W E V L I G V L V V S I L L L S	273
841	CTCCTCCTCTCCTCCAAACACTGGCGTCAGGGAAAACACAGGACATTGGCCCAG	900
274	L L L F L L Q H W R Q G K H R T L A Q	293
901	AGACAGGCTGATTCCAACGTCCAGGGCTGCCAGGCCAGAGCCAAAGGACGGGGC	960
294	R Q A D F Q R P P G A A E P E P K D G G	313
961	CTACAGAGGAGGTCCAGCCCAGCTGCTGACGTCCAGGGAGAAAATTCTGTGCTGCCGTG	1020
314	L Q R R S S P A A D V Q G E N F C A A V	333
1021	AAGGACACACAGCTGAGGACGGGTGAAATGGACACTCGGCAGAGCCCACACGATGAA	1080
334	K D T Q P E D G V E M D T R Q S P H D E	353
1081	GACCCCCAGGCAGTGACGTATGCCAAGGTGAAACACTCCAGACCTAGGAGAGAAATGCC	1140
354	D P Q A V T Y A K V K H S R P R R E M A	373
1141	TCTCCTCCCTCCCCACTGTCTGGGAATTCTGGACACAAAGGACAGACAGGCAGAAGAG	1200
374	S P P S P L S G E F L D T K D R Q A E E	394
1201	GACAGACAGATGGACACTGAGGTGCTGCATCTGAAGCCCCCAGGATGTGACTACGCC	1260
395	D R Q M D T E A A A S E A P Q D V T T P	413
1261	GGCTGCACAGCTTACCCCTCAGACAGAAGGCAACTGAGCCTCTCATCCCAGGAAGGG	1320
414	G C T A L P S D R R Q L S L L H P R K G	433
1321	CCTCTCCAGCTGAGCCCAGTGTCTATGCCACTCTGGCCATCCACTAATCCAGGGGGACC	1380
434	P L Q L S P V S M P L W P S T N P G G T	453
1381	CAGACCCCCACAAGCCATGGAGACTCAGGACCCCAGAAGGCATGGAAGCTGCCTCCAGTAG	1440
454	Q T P Q A M E T Q D P R R H G S C L Q *	472
1441	ACATCACTGAACCCAGCCAGCCCCACTGACACAGACCACTAGAAGATTCCGGAA	1500
1501	CGTTGGGAGTCACCTGATTCTGCAAAGATAATAATCCCTGCATTATC	1550

FIG. 10B

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Percent Similarity: 67.969 Percent Identity: 50.781

HMSHH46new.aa x FCg2RBos.aa

1 MIPTFTALLCLGLSLGPSTHMQAGPLPKPTLWAEPGSVISWGNSVTIWCQ 50  
| ||:.:|||||||:| .::|||.::|||.::|||:|||:|||:  
1 MAPTLPA LLCLGLSVGLRTQVQAGTFPKPIIWAEPSSVPLGSSVTILCQ 50  
  
51 GTLEAREYRLDKEESPAPWDRQNPLEPKNFKRFSIPSMTEDYAGRHYRCYY 100  
| . :....|:|||:...||: .|||.:|||. | .. |: ||||:| .  
51 GPPNTKSFSLNKEGDSTPWNIHPSLEPWDKANFFISNVREQQAGRHYCSH 100  
  
101 RSPVGWSQPSDPLELVMTGAYS.....KPTLSALPSPLVTSGKSVTLLC 144  
.|||:|||:|||:|||:|.. :|||. ||| |..|..|||:  
101 FIGVNWSEPSEPLDLLVAGEEPAGRLDRPSLSVRPSPSVAPGENVTLLC 150  
  
145 QSRSPMDTFLLIKERAHPLLHLRSEHGAQQHQAEFPMSPVTSVHGGTYR 194  
|| .. ||||| || |||. |:|||:.... .|||:.||| | .|||:  
151 QSGNRTDTFLSKEGAAHRPLRLRSQDGWYQAEFSLSPVTSAHGGTYR 200  
  
195 CFSSHGFSHYLLSHPSDPLELIVSGSLEGPRPSPTRSVSTAAGPEDQPLM 244  
|:..| : ..|||:|||:|||.||:| |: . | |:  
201 CYRSLSTNPYLLSQPSEPLALLV.....ADYTMQNL 232  
  
245 PTGSVPHSGLRRHWEVLIGVLVVSILLSLLLFLLLQHWRQGHRTLAQR 294  
. | |..|:||| :|: |:|:| ..|:  
233 RMG.....LAASVLLLGILL.....CQARHDHGAR 259  
295 QAD 297  
:|.  
260 EAA 262

**FIG. 11**

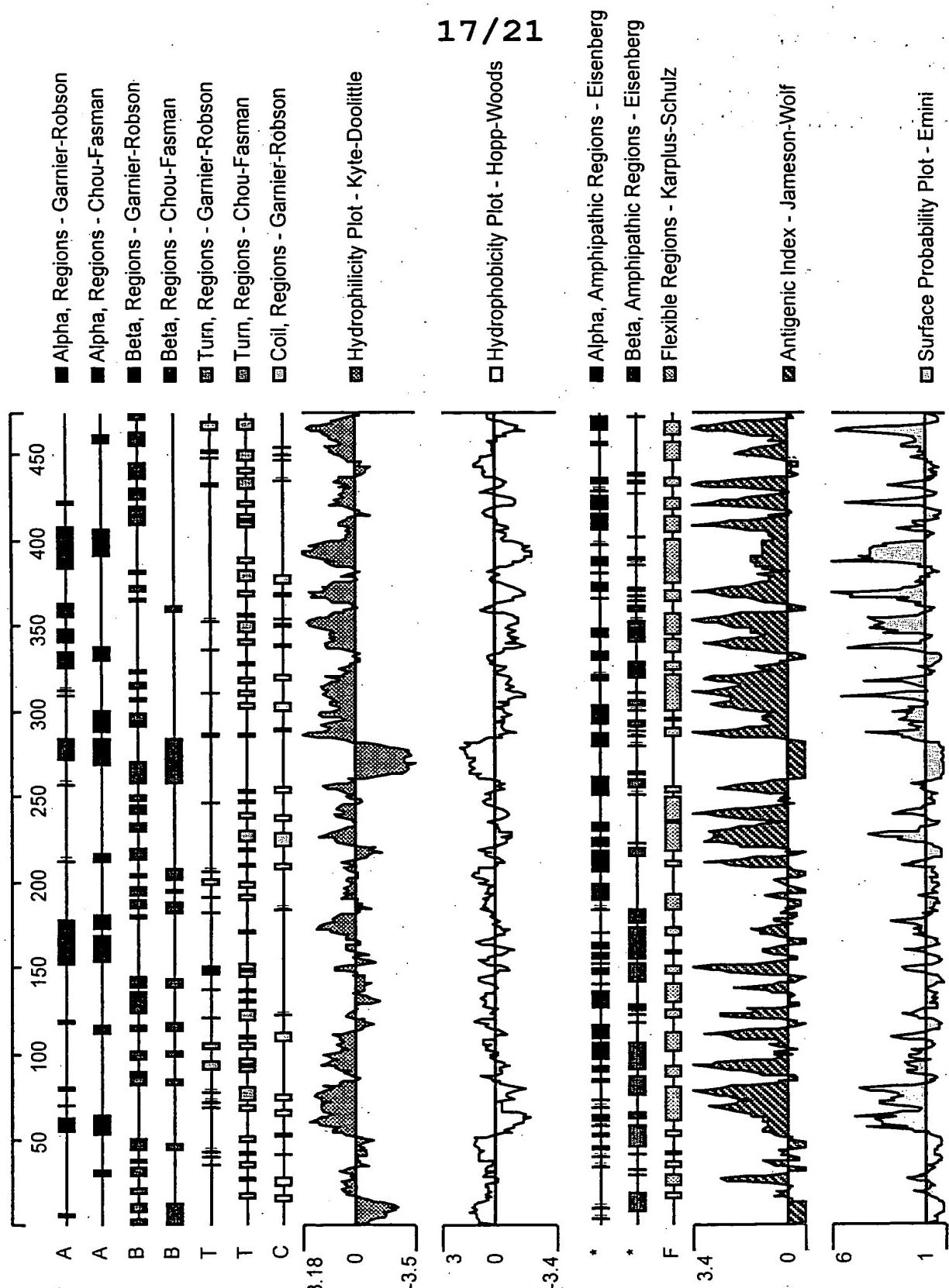


FIG. 12

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FcR-V

1	GCAGGAATTGGCACGAGCAGAGCAGGGCAGTGGGAGGAGACGCCATGACCCCCATCC	60
1	<u>M T P I L</u>	5
61	ACGGTCTGATCTGTCGGCTGAGTCTGGCCCCAGGACCCACGTGCAGGCAGGGCAC	120
6	<u>T V L I C L G L S L G P R T H V Q A G H</u>	25
121	CTCCCCAAGCCCACCTCTGGCTGAGCCAGGCTCTGTGATCATCCAGGAAAGTCTGTG	180
26	L P K P T L W A E P G S V I I Q G S P V	45
181	ACCTCAGGTGTCAGGGAGCCTCAGGCTGAGGAGTACCATCTATATAGGGAAAACAAA	240
46	T L R C Q G S L Q A E E Y H L Y R E N K	65
241	TCAGCATCTGGTTAGACGGATAACAAGAGCCTGGAAAGAATGGCAGTCCCCATCCA	300
66	S A S W V R R I Q E P G K N G Q F P I P	85
301	TCCATCACCTGGAACACGCAGGGCGGTATCACTGTCAGTACTACAGCCACAATCACTCA	360
86	S I T W E H A G R Y H C Q Y Y S H N H S	105
361	TCAGAGTACAGTGACCCCTGGAGCTGGTGGACAGGAGCCTACAGCAAACCCACCC	420
106	S E Y S D P L E L V V T G A Y S K P T L	125
421	TCAGCTCTGCCAGCCCTGTGGTACCTTAGGAGGGAACGTGACCCCTCCAGTGTCTCA	480
126	S A L P S P V V T L G G N V T L Q C V S	145
481	CAGGTGGCATTGACGGCTCATTCTGTGAAGGAAGGAGAAGATGAACACCCACAACGC	540
146	Q V A F D G F I L C K E G E D E H P Q R	165
541	CTGAACCTCCATTCCATGCCGTGGTGGCTGGCCATCTTCTCCGTGGCCCCGTG	600
166	L N S H S H A R G W S W A I F S V G P V	185
601	AGCCCGAGTCGCAGGTGGCTGACAGGTGCTATGCTTATGACTCGAACCTCCATGTG	660
186	S P S R R W S Y R C Y A Y D S N S P Y V	205
661	TGGTCTCTACCCAGTGTCTGGAGCTCTGGTCCAGGTGTTCTAAGAACCCATCA	720
206	W S L P S D L L E L L V P G V S K K P S	225
721	CTCTCAGTGCAGCCAGGTCTATGGTGGCCCTGGGAGAGCCTGACCCCTCCAGTGTGTC	780
226	L S V Q P G P M V A P G E S L T L Q C V	245
781	TCTGATGTCGGCTACGACAGATTGTTCTGTATAAGGAGGGAGAACGTGACTCCCTCAG	840
246	S D V G Y D R F V L Y K E G E R D F L Q	265

FIG. 13A

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**FcR-V**

841	CGCCCTGGTTGGCAGCCCCAGGCTGGGCTCTCCCAGGCCA	ACTTCACCCCTGGCCCTGTG	900
266	R P G W Q P Q A G L S Q A N F T L G P V		285
901	AGCCCCTCCCACGGGGGCCAGTACAGATGCTACAGTG	CACACAACCTCTCTCCGAGTGG	960
286	S P S H G G Q Y R C Y S A H N L S S E W		305
961	TCGGCCCCAGTGACCCCTGGACATCCTGATCACAGGA	CAGTTCTATGACAGACCCCTCT	1020
306	S A P S D P L D I L I T G Q F Y D R P S		325
1021	CTCTCGGTGCAGCCGGTCCCCACAGTAGCCCCAGGAAAGAAC	GCTGACCCCTGCTGTGTCAG	1080
326	L S V Q P V P T V A P G K N V T L L C Q		345
1081	TCACGGGGCAGTCCACACTTCTCTGACCAAGGAGGGGCAGGCC	ATCCCCACTG	1140.
346	S R G Q F H T F L L T K E G A G H P P L		365
1141	CATCTGAGATCAGAGCACCAAGCTCAGCAGAAC	CAGGCTGAATTCCGATGGTCCTGTG	1200
366	H L R S E H Q A Q Q N Q A E F R M G P V		385
1201	ACCTCAGCCCACGTGGGACCTACAGATGCTACAGCTCACTCAG	GTCCAACCCCTACCTG	1260
386	T S A H V G T Y R C Y S S L S S N P Y L		405
1261	CTGTCCTCTCCCAGTGACCCCTGGAGCTCGTGGTCTCAGCA	TCCAGGCCAACACCCC	1320
406	L S L P S D P L E L V V S A S L G Q H P		425
1321	CAGGATTACACAGTGGAGAATCTCATCCGATGGGTGTGGCTGG	CTGGTGGTC	1380
426	426 Q D Y T V E N L I R M G V A G L V L V V		445
1381	CTCGGGATTCTGCTATTGAGGCTCAGCACAGCCAGAGAAC	CTACAAGATGCAGCCGG	1440
446	L G I L L F E A Q H S Q R S L Q D A A G		465
1441	1441 AGTGAACAGCAGAGAGGACAATGCATCCTCAGCGTGGTGG	GAGCCTCAGGGACAGATCTG	1500
466	S E Q Q R G Q C I L Q R G G A S G T D L		485
1501	1501 ATGATCCCAGGAGGCTCTGGAGGACAATCTAGGACCTAC	ATTATCTGGACTGTATGCTGG	1560
486	M I P G G S G G Q S R T Y I I W T V C W		505
1561	1561 TCATTTCTAGAGACAGCAATCAATATTGAGTGTAA	GGAACTGTCTGGGTGATTCTA	1620
506	S F L E T A I N I *		514
1621	1621 GAAGATCATTAAACTGTGGTACATTTTTGTCTATG	1657	

**FIG. 13B**

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Percent Similarity: 70.722 Percent Identity: 55.513  
HMAAB68.aa x FCg2RBos.aa

1 MTPILTVLICLGLSLGPRTHVQAGHLPKPTLWAEPGSVIIQGSPVTLRCQ 50  
|.|.|..|:||||||:| ||:|||| :|||.|||:|||: || .|||: ||  
1 MAPTLPAALLCLGLSVGLRTQVQAGTFPKPIIWAEPSSVPLGSSVTILCQ 50  
  
51 GSLQAEYHLYRENKSASW.VRRIQEKGNGQFPIPSITWEHAGRYHCQY 99  
| . ....: | :|...|..| ::. || ...:| |..: ::|||||| .  
51 GPPNTKSFSLNKEGDSTPWNIHPSLEPWDKANFFISNVREQQAGRYHCSH 100  
  
100 YSHNHSSEYSDEPLELVTGAYSKPTLSALPSPVTLGGNVLQCVSQAF 149  
: ..|| |:||:|:|. |  
101 FIGVNWSEPSEPLDLLVAG..... 119  
  
150 DGFIILCKEGERDEHPQRLNSHSHARGWSWAI FSVGVPSPSRRWSYRCYAD 199  
:|.:|||. |  
120 .....EEPAGRLR..... 127  
  
200 SNSPYVWSLPSDLLELLVPGVKPKPSLSVQPGPMVAPGESLTQCVSDVG 249  
  
127 ..... 127  
  
250 YDRFVLYKEGERDFLQRPGWQPQAGLSQANFTLGPVSPSHGGQYRCYSAH 299  
  
127 ..... 127  
  
300 NLSSEWSAPS DPLDILITGQFYDRPSLSVQPVPTVAPGKNVTLLCQSRGQ 349  
|||||||. | .||||.||||||| ..  
128 .....DRPSLSVRPSPSVA PGENVTLLCQSGNR 155  
  
350 FHTFLLTKEGAGHPLLRLRSEHQAAQQNQAEFRMGPVTS A HVGTYRCYSSL 399  
.|||||.|||||:|.|||:|||:. |.. | |||.::|||||.|||||||.|||  
156 TDTFLLSKEGA AHRPLRLRSQDQDGWYQAEFSLSPVTS A HGGTYRCYRSL 205  
  
400 SSNPYLLSLPSDPLELVVSASLGQHPQDYT VENLIRMGVAGLVLVVLGIL 449  
|.|||||| |:||.|||. | |||:||||||:|: ||:||| |  
206 STNPYLLSQPSEPLALLVA.....DYTMQNLIRMGLAASVLLL GIL 247  
  
450 LFEAQHSQRSLQDAAGS 466  
| :|.|..: : .:|| |.  
248 LCQARHDHGGAREAARS 264

**FIG. 14**

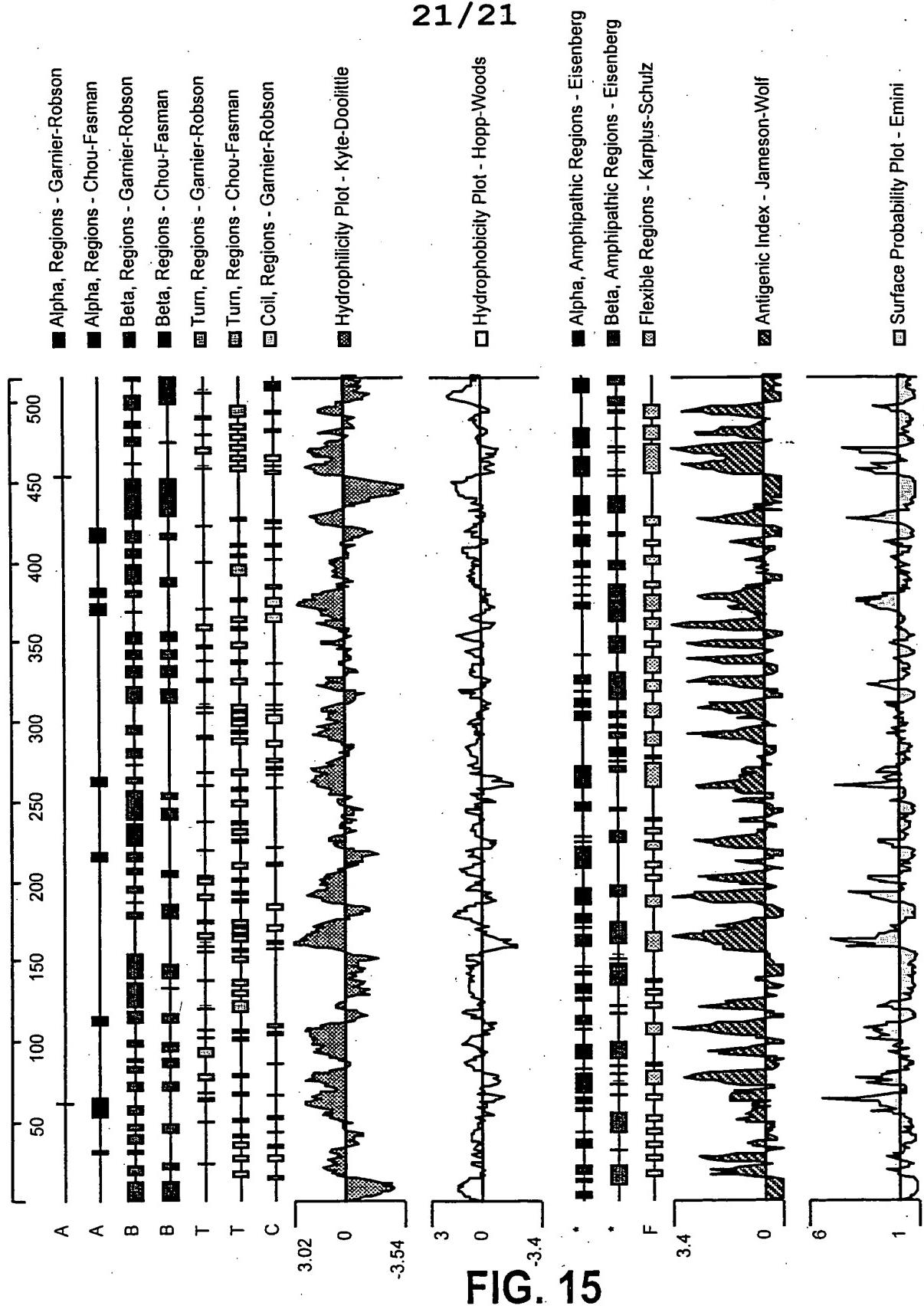


FIG. 15

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